were synthesized from the sequence of an EPSPS gene from Arabidopsis thaliana (Klee H.J. et al., (1987) Mol. Gen. Genet., 210, 437-442). These two oligonucleotides correspond to positions 1523 to 1543 and 1737 to 1717, respectively, of the published sequence and in convergent orientation.--

Please replace the paragraph beginning at page 13, line 3, with the following:

--Two single-stranded and partially complementary oligonucleotides of respective sequences (SEQ ID NO:10):

5'-AATTCCCGGG-3'

5'-CCCGGG-3' (the latter being phosphorylated)

are ligated to double-stranded cDNAs with blunt ends.--

Please replace the paragraph beginning at page 20, line 11, with the following:

--The plasmid DNA content of the various clones was analysed according to the procedure described for pRPA-ML-711. One of the plasmid clones retained contains an EcoRI-HindIII insert of about 1.45 kbp. The sequence of the terminal ends of this clone shows that the 5' end of the insert corresponds exactly to the corresponding end of pRPA-ML-711 and that the 3' terminal end has the following sequence (SEQ ID NO:11):

"5'...AATTAAGCTCTAGAGTCGACCTGCAGGCATGCAAGCTT-3'".--

Please replace the paragraph beginning at page 21, line 3, with the following:

--The clone pRPA-ML-712 was cut with the restriction enzymes PstI and HindIII. The DNA resulting from these manipulations was separated by electrophoresis on a 0.8 % LGTA/TBE agarose gel (ref. CPMB). The gel fragment containing the PstI/EcoRI insert of 1.3 kbp was excised from the gel and purified according to the procedure described in paragraph 5 above. This insert was ligated in the presence of an equimolar quantity of each of the two partially complementary oligonucleotides of sequence (SEQ ID NOS:12 and 13):

Oligo 1: 5'-GAGCCGAGCTCCATGGCCGGCGCCGAGGAGATCGTGCTGCA-3'

Oligo 2: 5'-GCACGATCTCCTCGGCGCCGGCCATGGAGCTCGGCTC-3'

as well as in the presence of DNA from the plasmid pUC19 digested with the restriction enzymes BamHI and HindIII.--

Please replace the paragraph beginning at page 24, line 16, with the following:

--The sequence of pRPA-ML-715 is arbitrarily numbered by placing the first base of the N-terminal alanine codon GCC in position 1. This sequence has an NcoI site in position 1217. The site-modifying oligonucleotide has the sequence (SEQ ID NO:14):

5'-CCACAGGATGGCGATGGCCTTCTCC-3'.--

Please replace the paragraph beginning at page 25, line 7, with the following:

--The following oligonucleotides (SEQ ID NOS:15, 16, 17 and 18) were used:

a) Thr 102 → Ile mutation.

5'-GAATGCTGGAATCGCAATGCGGCCATTGACAGC-3'

b) Pro 106 → Ser mutation.

5'-GAATGCTGGAACTGCAATGCGGTCCTTGACAGC-3'

c) Gly 101 → Ala and Thr 102 → Ile mutations.

5'-CTTGGGGAATGCTGCCATCGCAATGCGGCCATTG-3'

d) Thr 102 → Ile and Pro 106 → Ser mutations.

5'GGGGAATGCTGGAATCGCAATGCGGTCCTTGACAGC-3'--

Please replace the paragraph beginning at page 26, line 17, with the following:

--A DNA fragment of 418 base pairs is purified from digestion of the cosmid clone c22 with the restriction enzyme DdeI followed by treatment with a Klenow fragment of DNA polymerase from E. coli, according to the manufacturer's instructions for creating a blunt-ended DNA fragment and then cut with MseI. The purified DNA fragment is ligated to a synthetic oligonucleotide adaptor having the following sequence (SEQ ID NOS:19 and 20):

Adaptor 1: 5' TAATTTGTTGAACAGATCCC 3'

TAAACAACTTGTCTAGGG--

Please replace the paragraph beginning at page 27, line 5, with the following:

--3. Intron No. 2:

A DNA fragment of 494 base pairs is purified from the digestion of the cosmid clone c22 with the restriction enzymes AluI and CfoI. The purified DNA fragment is ligated to a synthetic oligonucleotide adaptor having the following sequence (SEQ ID NOS:21 and 22):